

Fig. 1A

1 GGCACGAGGC AAGCCTTCCA GGTATCTGTC ACGCACCCTTG AAGTCTGAG AGCTACTGCC CTACAGAAG TTACTAGTGC CCTAAGCTG GCGCTGGCAC
CCGTGCTCCG TTCGGAAGGT CCAATAGCAC TGCCTGGAAC TTTCAGACTC TCATGACAGG GATGCTTTC AATGATCAGC GGATTTCGAC CGCGACCGTG
^start insert

101 TGATGTTACT GCTGCTGTTG GAGTACAAC TCCCTATAGA AAACAACCTGC CAGCACCCTTA AGACCCTCA CACCTTCAGA GTGGCCTTGA GAAAGATTG
ACTACATGA CGACGACAC CTCATGTTGA AGGATATCT TTGTTGACG GTCGTGAAT TCTGGTAGT GTGAAGCTT CACCGGAAC CTTCCTAAC
1 M L L L L L E Y N F P I E N N C Q H L K T T H T F R
^Met
^possible splice donor

201 GGGTCAAGGA TCATGAGCGA GAACACCCT TAAGAGATA GTGAAGTGT CTGCATGTGA GACGCTGAGA TCCTATGTCA GGCTGTGATA GGAGGAAAC
CCGAGTTCT AGTACTCGCT CTGTGTGTGA ATTCTCTAT CACTGTATCA GACGTACACT CTGCGACTCT AGGATACAGT CCGACACTAT CTCTCCTTG

301 AGAAACCAAA GGAAGAACA GCTTTAAGA GCGCTTAAGA GCCACCACC CATTCTGAC AGTCACTGGC CCAGCCTGGG GGGCCCTGTT CTTCATCAAA
TCTTGGTTT CTTTCTTGT CGAATTCTT CGGAGTTCT CGTGGGTGG GTAGAAGCTG TCAGTGACCG GGTGGACCC CCGGGACAA GAAATAGTTT

401 CAAGTCCCTG AGCTCTTTCG AGAGTCCAA AGGTGAAGA CTTAACCCG AAGAATTCA GCATTCAATGA CCAGATCAC AAAGTACTGG TCCTGACTC
GTTCAAGGAC TCGAGAAACG TCTCCAGGTT TCCACTTCTT GAATTTGGGC TTCTTTAAGT CTAAGTACT GTTCTAGTG TTTCATGACC AGGACTGAG
1 V K N L N P K K F S I H D Q D H K V L V L D S

^85066.AH1282.Asc.f, 5'Tag: TTTCCCTTTGGCGCGCC
^85066.AH1284.Nsi.f, 5'Tag: TTTCCCTTTATGATCATGATGACATGACAA

^possible splice acceptor
^ORF

501 TGGGATCTC ATAGCAGTTC CAGATAAAAA CTACATACGC CCAGAGATCT TCTTTGCATT AGCCTCATCC TTGAGCTAG CTTCTGCGGA GAAAGAGT
ACCTTAGAG TATGTCAGG GTCTATTTT GATGTATGG GGTCTTAGA AGAACGTAA TCGAGTAGG AACTGAGTC GGAGACGCT CTTCCTTCA
24 G N L I A V P D K N Y I R P E I F F A L A S S L S S A S A E K G S

601 CCGATTCTCC TGGGGTCTC TAAAGGGAG TTTTGTCTT ACTGTGCAA GGATTAAGGA CAAATCAATC CATCCCTTCA GCTGAAGAG GAGAACTGA
GGCTAAGAG ACCCCAGAG ATTCCCTCC AAAACAGAGA TGACACTGTT CTAATTTCT GTTTCAGTAG GTAGGAGAT CGACTTCTT CTCTTTGACT
57 P I L L G V S K G E F C L Y C D K D K G Q S H P S L Q L K K E K L M

701 TGAAGCTGGC TGCCCAAAAG GAATCAGCAC GCCGGCCCTT CATCTTTTAT AGGCTCAGG TGGGCTCCTG GAACATGCTG GAGTCGGCGG CTCACCCCGG
 ACTCGACCG ACGGTTTTC CTTAGTCGTG CGGCCGGGAA GTAGAAATA TCCGAGTCC ACCGAGGAC CTTGTACGAC CTCAGCCGCGG GAGTGGGGCC
 91 K L A A Q K E S A R R P F I F Y R A Q V G S W N M L E S A A H P G
 801 ATGTTTCATC TGCACCTCCT GCAATTGTAA TGAGCTGTT GGGGTGACAG ATAAATTGA GAACAGGAAA CACATTGAAT TTTCATTCA ACCAGTTGC
 TACCAAGTAG ACGTGAGGA CGTTAACATT ACTCGGACAA CCCCACTGC TATTTAACT CTTGTCCTT GTTTAACTTA AAGTAAGT TGGTCAACG
 124 W F I C T S C N C N E P V G V T D K F E N R K H I E F S F Q P V C
 901 AAAGCTGAAA TGAGCCCCAG TGAGTTCAGC GATTAGAAA CTGCCCATT GAACGCTTC CTCGTAATT TGAACATAAT GTATAAAAC ACCAACTG
 TTTCGACTTT ACTCGGGGTC ACTCCAGTCG CTATTCCTTT GACGGGGTAA CTGCGGAAG GAGGATTA ACTTGATTAA CATATTTTGG TGGTTGGAC
 157 K A E M S P S E V S D O
 ^85066.AH1283.r
 ^85066.AH1285.NoI.r, 5'Tag: TTTCCTTTGCGCGCCTTA
 1001 CTCACT
 GAGTGA

Fig 1B

Fig 2

```
1 TAAATCACC A TGCTGCACT TCTGATCCTA GCTCTTGTTG GAGCTGCAGT TCCTGACTAC AAAGACGATG ACGACAAGCT TCGGCGCCGG AATTGAGCTC
1 AATTAGTGT ACAGACGTGA AGACTAGAT CGAGAACAAC CTCGACGTCA ACGACTGATG TTCTGCTAC TGCTGTTGA ACGCGCGCGC TTAAGTCAG
1 M S A L L I L A L V G A A V A D Y K D D D D K L A A A N S A L
^orf ^flag ^insert st
101 TTTCGAGAGG TCCAAAGTG AAGACTTAA ACCCGAAGA ATTGACATT CATGACCAGG ATCACAAGT ACTGTCTG GACTGTGGA ATCTCATAGC
AAAGCTCTCC AGGTTCCAC TTCTGAATP TGGGCTTCTT TAAGTCGTA GTAGTGTC TACTGTTTCA TGACCAGAC CTGAGACCTT TAGAGTATCG
32 C R G P K V K N L N P K K F S I H D Q D H K V L V L D S G N L I A
201 AGTTCCAGAT AAAAATACTA TACGCCCAAG GATCTTCTTT GCATTAGCCT CATCCTTGAG CTCAGCCTCT GCGGAGAAAG GAAGTCCGAT TCTCCTGGGG
TCAAGGTCTA TTTTGTATG ATGCGGGTCT CTAGAAGAA CGTATCGGA GTAGGAAGTCT ZAGTCGAGA CGCCTCTTTC CTTGAGGCTA AGAGGACCCC
65 V P D K N Y I R P E I F F A L A S S L S S A S A E K G S P I L L G
301 GTCTCTAAG GGGAGTTTG TCTTACTGT GACAAGATA AAGACAAG TCATCCATCC CTTGAGCTGA AGAAGAGAA ACTGATGAG CTGGCTGCCC
CAGAGATTTC CCTCAAAAC AGAGATGACA CTGTTCTAT TTCTGTTTC AGTAGTAGG GAAGTCGACT TCTTCTCTT TGACTACTTC GACCGACGGG
98 V S K G E F C L Y C D K D K G Q S H P S L Q L K K E K L M K L A A Q
401 AAAAGATC AGCAGCCCG CCTTCACTT TTTATAGGGC TCAGGTGGG TCCTGAGACA TGCTGAGTC GCGGCTCAC CCCGATGCT TCATCTGAC
TTTTCCTTAG TCGTGCGCC GGAAGTAGA AAATATCCG AGTCCACCCG AGGACCTGT AGGACCTCAG CCGCGAGTG GGGCTTACA AGTAGACGTG
132 K E S A R R P F I F Y R A Q V G S W N M L E S A A H P G W F I C T
501 CTCCTGCAAT TGTATGAGC CTGTTGGGT GACAGATAAA TTTCGAGACA GGAACACAT TGAATTTTCA TTTCACCCAG TTTCGAAAGC TGAATGAGC
GAGGACGTTA ACATTACTCG GACAACCCA CTGTCTATTT AAACCTTGT CTTTGTGTA ACTTAAGT AAAGTTGTC AAACGTTTC ACTTTACTCG
165 S C N C N E P V G V T D K F E N R K H I E F S F Q P V C K A E M S
601 CCCAGTGAG TCAGCGATT GGTATCAGT CGACTCTAGA GGATCCCGGG
GGGTCACTCC AGTCGTAAT CCCATGCTCA GCTGAGATCT CCTAGGGCCC
198 P S E V S D O
^inserts ends
```

1 GGCACGAGGC AAGCCTTCCA GGTATATCTG ACGCACCTTG AAAGTCTGAG AGCTACTGCC CTACAGAAG TTACTAGTGC CTTAAGCTG GCGCTGGCAC
CCGTGCTCCG TTCGGAAGGT CCAATAGCAC TGCGTGGAAC TTTCAGACTC TCGATGACGG GATGCTTTTC AATGATCAGG GGATTTCGAC CGCGACCGTG

101 TGATGTTACT GCTGCTGTTG GAGTACAAC TCCCTATAGA AAACAACCTGC CAGCACCTTA AGACCACCTCA CACCTTCAGA GTGAAGAAT TAAACCCGAA
ACTACATGA CGACGACAACT CTCATGTTGA AGGATATCT TTTGTTGACG GTGCTGGAAT TCTGTTGAGT GTGAAGTCT CACTTCTTGA ATTGGGCTT
1 M L L L L L E Y N F P I E N N C Q H L K T T H T F R V K N L N P K
Met

201 GAAATTCAGC ATTATGACC AGATCACAAG AGTACTGCTC CTGCACTCTG GGAATCTCAT AGCAGTTCCA GATAAAACT ACATACGCC AGAGATCTTC
CTTTAGTGC TAACTACTGC TCCTAGTGT TCAATGACCAAG GACCTGAGAC CCTTAGAGTA TCGTCAAGT CTATTTTGA TGTATGCGGG TCTCTAGAAG
34 K F S I H D Q D H K V L V L D S G N L I A V P D K N Y I R P E I F

301 TTTCATTTAG CCTATCCTT GAGCTCAGCC TCTGCGGAGA AAGGAAGTCC GATTCTCTCTG GGGTCTCTA AAGGGAGTT TTGCTCTAC TGTGACAAGG
AAACGTAATC GGAGTAGGAA CTCGAGTCGG AGACGCTCTT TTCTTTCAGG CTAAGAGGAC CCCAGAGAT TTCCCTTCAA AACAGAGATG ACACTGTTCC
67 F A L A S S L S S A S A E K G S P I L L G V S K G E F C L Y C D K D

401 ATTAAGGACA AAGTCATCCA TCCCTTCAGC TGAAGAAGA GAACTGATG AAGCTGGCTG CCCAAAAGA ATCAGCAGCG CGGCCCTTCA TCTTTTATAG
TATTTCTGT TTCAGTAGT AGGAGATCG ACTTCTTCTT CTTTGACTTAC TTCAGCCGAC GGGTTTCTT TAGTCGTGCG GCCGGGAAGT AGAAATATC
101 K G Q S H P S L Q L K K E K L M K L A A Q K E S A R R P F I F Y R

501 GGCTCAGTGG GGCTCCTGGA ACAATCTGGA GTGCGCGGCT CACCCCGGAT GGTTCATCTG CACCTCCTGC AATTGNAATG AGCTGTGCG GGTGACAGAT
CCGAGTCAC CCGAGGACCT TGTACGACCT CAGCCGCCGA GTGGGGCTTA CCAAGTAGAC GTGAGGACG TTAACATTTAC TCGACACAAC CCACTGTCTA
134 A Q V G S W N M L E S A A H P G W F I C T S C N C N E P V G V T D

601 AAATTGAGA ACAGGAACA CATTGAATTT TCATTTCAC CAGTTTGCAA AGCTGAATG AGCCCGAGTG AGGTACGGA TTAGGAACCT GCCCATTTGA
TTTAACCTCT TGTCTTTTGT GTAACCTTAA AGTAAAGTTG GTCAACGTT TCGACTTAC TCGGGTAC TCCAGTCCGT AATCCTTTGA CCGGTAAC
167 K F E N R K H I E F S F Q P V C K A E M S P S E V S D O

701 ACGCCTTCTT CGCTAATTTG AACTAATGT ATAAAAACAC CAAACCTGCT CACT
TCCGGAAGA GCGATTAAAC TTGATPACA TATTTTGTG GTTGGACGA GTGA

Fig 4

1 CCAGGCCCAA GCNCCCAC CATGAATTT GTTCACACAA CTCGAAGGT GAAGACTTA AACCCGAAGA AATTCAGCAT TCATGACCAG GATCACAAG
GGTCCGGGTT CGNAGGGGTG GFACTTAAA CAAGTGTGTT CAGCTTCCA CTCTCGAAT TTGGGCTTCT TTAAGTCGTA AGTACTGTC CTAGTGTTC
101 TACTGGCCTG GACTCTGGGA ATCTCATAGC AGTTCAGAT AAAACTACA TACGCCAGA GATCTCTTT GCATTAGCCT CATCCTTAG CTCAGCCTT
ATGACCGGAC CTGAGACCTT TAAAGTATCG TCAAGTCTA TTTTGATGT ATGCGGCTCT CTAGAGAAA CGTAATCGGA GTAGGAATC GATTCGAGA
201 GCGGAGAAAG GAAGTCCGAT TCTCCTGGGG GTCTCTAAG GGGAGTTTG TCTCTACTGT GACAAGATA AAGACAAG TCATCCATCC CTCAGCTGA
CGCCTCTTTC CTTCAGGCTA AGAGGACCCC CAGAGATTTC CCTCAAAAC AGAGATGACA CTGTCTTAT TTCTGTTC AGTAGTAGG GAAGTCGACT
1 I L L G V S K G E F C L Y C D K D K G Q S H P S L Q L K
^orf
^84664.f1
^84664.p1
301 AGAAGAGAA ACTGATGAAG CTGGCTGCCC AAAAGAATC AGCAGCCCG CCTTCATCT TTTATAGGC TCAGGTGGC TCCTGACA TGCTGAGTC
TCTTCTCTT TGACTACTTC GACCGACGGG TTTTCTTAG TCGTGGCGC GGAAGTAGA AAATATCCCG AGTCCACCCG AGGACCTGT ACGACCTCAG
29 K E K L M K L A A Q K E S A R R P F I F Y R A Q V G S W N M L E S
401 GCGGCTCAC CCCGATGAT TCATCTGCAC CTCTGCAAT TGTATGAGC CTGTGGGGT GACAGATAA TTGAGACA GGAACACAT TGAATTTCA
CCGCCGATG GGGCTACCA AGTAGACGTG GAGACGTTA ACATTAATCG GACAACCCA CTGTCTATTT AAACCTTGT CCTTGTGTA ACTTAAAGT
62 A A H P G W F I C T S C N C N E P V G V T D K F E N R K H I E F S
501 TTTCAACCAG TTTGCAAGC TGAATGAGC CCCAGTAGG TCAGCGATTA GGAAGTCCC CCAATTGAAG CCTTCCTGCG TAATTGAGC TAATTGTATA
AAAGTTGCT AAAGCTTTCG ACTTACTCG GGGTCACTCC AGTCGTAAT CCTTGACGG GGTAACTTGC GGAAGAGCG ATTAACCTTG ATTAACATAT
95 F Q P V C K A E M S P S E V S D O
^84664.r1
601 AAAACCCCAA ACCTGCTCAC TAAAAAAA
TTTTGGGGTT TGGACGAGTG ATTTTTTTT

Fig 5A

1 GTGACCCAC GCGTCCGAAG CTGCTGAGC CACGATTCAG TCCCTGGAC TGTAGATAA GACCCCTTCT TCCAGGTGC TGAGACAACC ACACATGAG
CAGCTGGGTG CGCAGGCTTC GACGACCTCG GTGCTAAGTC AGGGACCTG ACATCTATT CTGGGAAGA ACGTCCACG ACTCTGTG TGTGATCTC
1
^insert starts M R
^MET

92929.AH1421.Asc.f, 5' Tag: AAAGGAAAGCGCGCC^

101 AGGCACTCCA GGAGCGCTG ATGTGAGG AAGGCGCTC TATCAATCAA TCACCTGTGC TGTATACACA TGCAAGTATC CAGAGCTCT TGAGCAAGGC
TCCGTGAGGT CCTCTGCGAC TACCACCTCC TTCCCGGCGAG ATAGTTAGTT AGTGACAACG ACAATAGTGT ACGTTCATAG GTCTCCGAGA ACTCGTTCCG
3 G T P G D A D G G G R A V Y Q S I T V A V I T C K Y P E A L E Q G
201 AGAGGGGATC CCATTATTTT GGAATCCAG AATCCAGAAA TGTGTTGTA TTGTGAGAAG GTTGAGAAG AGCCACATT GCAGCTAAAA GAGCAGAGA
TCTCCCTTAG GGTAAATAAA CCTTAGTTC TTAGGTCTTT ACACAACAT AACACTCTTC CAACCTCTTG TCGGTGTAA CGTCATTTT CTGCTCTCT
36 R G D P I Y L G I Q N P E M C L Y C E K V G E Q P T L Q L K E Q K I
301 TCATGGATCT GTATGGCCAA CCCGAGCCG TGAACCTT CCTTTCTAC CGTGCCAAGA CTGCTAGGAC CTCACCCCTT GAGTCTGTGG CCTTCCCGGA
AGTACCTAGA CATACCGGTT GGGCTCGGC ACTTTGGAA GGAAGAAGATG GCACGGTTCT GACCATCTCG GAGTGGGA CTCAGACACC GGAAGGCCCT
70 M D L Y G Q P E P V K P F L F Y R A K T G R T S T L E S V A F P D
401 CTGCTTCATT GCCTCCTCCA AGAGAGACCA GCCCATCATT CTGACTTCAG AACTTGGAA GTCATACAC ACTGCCCTTG AATTAAATAT AAATGACTGA
GACCAAGTAA CGGAGAGGT TCTCTCTGTT CGGTAGTAA GACTGAAGTC TTGAACCTT CAGTATGTTG TGACGGAAC TTAATTATTA TTACTGACT
103 W F I A S S K R D Q P I I L T S E L G K S Y N T A F E L N I N D O
^92929.AH1
501 ACTCAGCCTA GAGTGGCAG CTYGTCTTT GTCTTAAAGT TTCTGTCTCC CAATGTGTTT TCGCTACAT TTCTTAAAGT TCAATTTTAC GCTGTGCTG
TGAGTCGAT CTCACCGTC GAACAGAAA CAGATTTC AAGCCAAG GTTACACAA AGCAGATGA AAAGATCAC AGTAAAGTG CGACCACGAC
136
601 AGACAGAGC AAGCTGCTG TTATCATCTC ATTTTATAT GAAGAAGAG CAATTACTTC ATAGCAACTG AAGAACAAGA TGTGGCTCA GAAGCAGAG
TCTGTCTCG TTCCGACGAC AATAGTAGAG TAAATATTA CTCTCTCTC GTTAATGAG TATCGTTGAC TTCTTGTCT ACACCGAGT CTTCGTCTC
701 AGCTGGGTG TATAAGCTG TCCCTCAAG CTGTGCTGT GTAGGCCACA AGGCATCTGC ATGAGTACT TTAAGACTCA AAGACCAAC ACTGACTTT
TCGACCCACC ATATTCCGAC AGAGAGTTT GACCAGACA CATCCGGTGT TCCGTAGAG TACTCACTGA AATTCTGAGT TTCTGTGTTG TGACTCGAAA

801 CTCTAGGGG TGGGTATGAA GATGCTTCAG AGCTCATGCG CGTTACCCAC GATGGCATGA CTAGCACAGA GCTGATCTCT GTTCTGTGTT TGCTTTATTC
 GAAGATCCCC ACCCATACTT CTACGAAGTC TCGAGTACGC GCAATGGGTG CTACCGTACT GATCGTGTCT CGACTAGAGA CAAAGACATA ACGAATATAG
 901 CCTCTGGGA TGATATCATC CAGTCTTTAT ATGTGCGCAA TATACCTCAT TGTGTATAT AGAACCTTCT TAGCATTAAG ACCTTGTAAA CAAAAATAAT
 GGAGAACCCCT ACTATATAGTAG GTCAAGAAATA TACAACGGTT ATATGGAGTA ACACACATTA TCTTGGAAGA ATCGTAATTG TGAACATTTT GTTTTATTTA
 1001 TCTTGGGGTG GGTATGAAGA TGCTTCAGAG CTCATGCGGG TTACCCACGA TGGCATGACT AGCACAGAGC TGATCTCTGT TTCTGTGTTG CTTTATTCCT
 AGAACCCCCAC CCATCTTCT ACGAAGTCTC GAGTACGGCG AATGGGTGCT ACCGTACTGA TCGTGTCTCG ACTAGAGACA AAGACAATAAC GAAATAGGGG
 1101 TCTTGGGATG ATATCATCCA GTCTTTATAT GTTGCCAATA TACCTCATG TGTGTATATG AACCTTCTTA GCATTAGAC CTTGTAAACA AAAATTAATC
 AGAACCCCTAC TATATAGGT CAGAAATATA CAACGGTTAT ATGAGTAAC ACACATTATC TTGGAAGAAT CGTAATTCTG GAACATTTGT TTTTATTAAG
 1201 TTGTGTTAAG TTAATCATTT TTTGTCCATA TTGTAATGTG TAATCTTAAA GTTAATAATA CTTTGTGTAT TTATATAATA ATAAAGCTAA AACGATATA
 AACACAATTC AATTAGTAA AAACAGGATT AACATTACAC ATTAGAATTT CAATTTATTT GAACACATAA AATATATTAT TATTTGCAAT TTGACTATAT
 1301 AAATAAAGAA AGAGTAAACT G
 TTTATTTCTT TCTCATTTGA C

Fig 5B

Fig. 6

1 AAGTGTCTGG AGCCACGATT CAGTCCCCCTG GACTGTAGAT AAAGACCCTT TCTTGCCAGG TGCTGAGACA ACCACACTAT GAGAGGCACT CCAGAGACG
TTCGACGACC TCGGTGCTAA GTCAGGGGAC CTGACATCTA TTTCTGGGAA AGAAGGTCC ACGACTCTGT TGGTGTGATA CTCTCCGTGA GGTCCCTCTGC
101 CTGANGGTGG AGAAGGGCC GTCTATCAAT CAATCACTGT TGCTGTTATC ACATGCAAGT ATCCAGAGGC TCTTGAGCAA GGCAGAGGGG ATCCCATTTA
GACTACCACC TCCTTCCCGG CAGATAGTTA GTTAGTGACA ACGACAATAG TGTACGTCA TAGGTCTCCG AGAACTCGTT CCGTCTCCCC TAGGTAAT
201 TTTGGGAATC CAGAATCCAG AAATGTGTTT GTATTGTAG AAGTTTGA
AAACCCTTAG GTCTTAGGTC TTTACACAAA CATAACACTC TTCCAACCT

Fig 7

1 ATGATCCTGA GTGGGCGCT GTGCTTCGA ATGAAGACT CGGATTTGA GGTGCTTAT CTGCATAATA ACCAGCTTCT AGCTGAGGG CTGCATGCAG
TACCAGACT CACCCCGCGA CACGAAGCT TACTTCCTGA GCCGTAATTT CCACGAATA GACGTATTTT TGTGCAAGA TCGACCTCCC GACGTACGTC
1 M V L S G A L C F R M K D S A L K V L Y L H N N Q L L A G G L H A G
101 GGAAGTCAT TAAAGTGAA GAGATCAGC TGTGCCCAA TCGTGGCTG GATGCCAGCC TGTCCCCCGT CATCCTGGGT GTCCAAGGTG GAAGCCAGTG
CCTTCAGTA ATTTCACCTT CTCTAGTCGC ACCAGGGGT AGCCACCGAC CTACGGTCG ACAGGGGCA GTAGACCCA CAGTCCAC CTTCGGTCA
35 K V I K G E E I S V V P N R W L D A S L S P V I L G V Q G G S Q C
201 CCTGTCAATG GGGTGGGCG AGAGCCGAC TCTAACACTA GAGCCAGTGA ACATCATGGA GCTCTAATTT GGTGCCAAGG AATCCAAGAG CTTCACCTTC
GGACAGTACA CCCACCCCG TCCTGGGCTG AGATTGTGAT CTGGTCACT TGTAGTACCT CGAGATAGAA CCACGGTTCC TTAGTTCTC GAACTGGAAG
68 L S C G V G Q E P T L T L E P V N I M E L Y L G A K E S K S F T F
301 TACCGGCGG ACATGGGCT CACCTCCAGC TTGAGTCGG CTGCTTACCC GGGCTGTTT CTGTGACAGG TGCTGAAGC CGATCAGCCT GTTCAGACTCA
ATGCCGCCC TGTACCCCGA GTGAGGTG AGCTCAGCC GACGATGGG CCCGACCAAG GACACGTGCC ACGACTTCG GCTAGTCGA CAGTCTGAGT
101 Y R R D M G L T S S F E S A A Y P G W F L C T V P E A D Q P V R L T
401 CCCAGCTTCC CGAATGCT GGTGGAATG CCCCATCAC AGACTTCTAC TTCCAGCAGT GTGACTAG
GGTGAAGG GCTCTTACA CCGACTTAC GGGGTAGTG TCTGAAGATG AAGTGTCA CACTGATC
135 Q L P E N G G W N A P I T D F Y F Q Q C D O

1 GCTCCCGCCA GGAGAAAGGA ACAATTCTGAG GGGAGTCTAC ACCCTGTGGA GCTCAAGATG GTCTGAGTG GGGCGCTGTG CTTCCGAATG AAGACTCGG
 CGAGGGCGGT CCTCTTCTCT TGTAGACTTC CCTTCAGATG TGGACACCTT CGAGTTCTAC CAGACTTCAC CCGCGACAC GAAGGCTTAC TTCTGAGCC
 1 A P A R R K E H S E G S L H P V E L K M V L S G A L C F R M K D S A
 101 CATGAAGGT GCTTTATCTG CATATAACC AGCTTCTAGC TGGAGGCTG CATGCAAGGA AGGTCAATTAA AGGTGAAGAG ATCAGCGTGG TCCCATATCG
GTAATTCCA CGAATAGAC GTATTATTGG TCGAAGATCG ACCTCCCGAC GTACGTCCCT TCCAGTAATT TCCACTTCTC TAGTCGCACC AGGGTTAGC
 35 L K V L Y L H N N Q L L A G G L H A G K V I K G E E I S V V P N R
 201 GTGGCTGGAT GCCAGCCTGT CCCCCGTCAAT CTTGGGTGTC CAGGTGGA GCCAGTGCCT GTCAATGTTGG GTGGGGCAGG AGNCGACTCT AACAT
 CACCGACCTA CGGTGGACA GGGGGCAGTA GACCCACAG GTCCACACTT CGTCAAGGA CAGTACACCC CACCCGCTCC TONGTGAGA TTGTA
 68 W L D A S L S P V I L G V Q G G S Q C L S C G V G Q E X T L T

Fig 9A

1 ATAGGGAATT TGGCCCTCGA GGCCAAGAAT TCGCAGCAG GGAGCCCTGC TTTCCTACTTA GGTCTCAAT TTTCAGCCT TGTCTTGGC TAAATTTCC
TATCCCTTAA ACCGGAGCT CCGTCTCTTA AGCCGTGCTC CCTTCGACG AAAGATGAAT CCAGAGTTA AAAGTCCGA ACAGAACCG ATTTTAAAGG
^insert starts

101 TGCTGTTTAT TTCAAAATAG GGTCTACATA CTGTGAGCT CATGATGTT CTGAGTGGG CACTATGCTT CCGAATGAAG GATTACGCT TGAAGTACT
ACGACAATA AAGTTTATC CCAGATGAT GACACCTCGA GTACTACCA GACTCACCC GTGATACGAA GGCTTACTTC CTAGTCCGA ACTTCATGA
1
M V L S G A L C F R M K D S A L K V L
^orf

201 GTATCTGCAC AATAACCAGC TGCTGGCTGG AGGACTGCAC GCAGAGAAGG TCATTTAAGG TGAGGAGATC AGTGTGTCC CAAATCGGC ACTGATGCC
CATAGACGTG TTATTTGTCG ACGACCGACC TCCTGACGTG CGTCTCTCC AGTAATTTCC ACTCCTCTAG TCACACACAG GTTTAGCCG TGACCTACGG
20 Y L H N N Q L L A G G L H A E K V I K G E E I S V V P N R A L D A

301 AGTCTGTCCC CTGTCATCCT GGGCGTTCAA GGAGGAACC AGTCCCTATC TTGTGGGACA GAGAAAGGC CAATTCTGAA ACTTGAGCCA GTGAACATCA
TCAGACAGGG GACAGTAGA CCGCAAGTT CCTCCTTCGG TCACGATAG AACACCTGT CTCTTTCCC GTTAAGACTT TGAATCGGT CACTGTGAGT
53 S L S P V I L G V Q G G S Q C L S C G T E K G P I L K L E P V N I M

401 TGGAGCTCTA CCTCGGGGCC AAGAATCAA AGAGCTTCAC CTTCACCGG CCGGATATGG GTCTTACCTC CAGCTTCGAA TCCGCTGCCT ACCGAGGCTG
ACCTCGAGAT GGAGCCCCG TTCTTACTT TCTCGAAGTG GAAGATGGCC GCCCTATACC CAGATGGAG GTCGAAGCTT AGCGACGGA TGGTTCGAC
87 E L Y L G A K E S K S F T F Y R R D M G L T S S F E S A A Y P G W

501 GTTCCTCTGC ACCTCACCGG AAGCTGACCA GCCTGTACAG CTCACCTCAGA TCCCTGAGGA CCCCAGCCTGG GATGCTCCCA TCACAGACTT CTACTTTACG
CAAGAGACG TGGAGTGCC TTGCACTGCT CGGACAGTCC GAGTGAAGTCT AGGGACTCCT GGGCGGACC CTACGAGGCT AGTGTCTGAA GATGAAGTC
120 F L C T S P E A D Q P V R L T Q I P E D P A W D A P I T D F Y F Q

601 CAGTGTGACT AGGCTGCGT GGTCCCAAA ACTCCATTAAG CAGAGGCAGA GTAGGCAGTG GCGGCTCCTG ATAGAGATA GAGAGACAGA GGAGCTCCAC
GTACACTGA TCCGACGCA CCAGGGGTTT TGAGTATTC GTTCCTCTCT CATCCGTAC CGCCGAGAC TATCTCTAT CTCTCTGCT CCTGAGGTG
153 Q C D O

701 AGTAGTGGC TTAATCTCTT CCTTCCCTAC TGACTTCCCG CTTCGACCT AAGGCACACA GACACTCTT TCTCTGCAAT CCCAGTCTG GTAATCTTC
TCATCCACCG AATGAGAGA GGAAGGATG ACCTGAGGGC GAAAGACTGA TTCCGTGTGT CTGTGAGAGA AGAGAGCTA GGTTCACGAC CATTTAGAAG

801 TGGTATTG AGCTCAATGT GTAGATTCTT TCAGATTGGA TGGTACTACC TCTGTGTGG AACCAATAG AACCAAGTA GGACCAACA AGAGCAACAT
 ACCATAAAC TCGAGTTACA CATCTAAGAA AGCTAACCT ACCATGATGG AGACCACACC TTGGGTATC TTGTGTGAT CCGGTGTGTT TCTGCTTGT
 901 AAAAGATTCT TGGTGAAGA AGAGTGGGA ACTGTTTATA CATAGTAAGA TCTGACACAG TACCTCAGAA GTCCCTGCCAT TCCATTATGTT CTGAGAAAG
 TTTTCTAAGA ACCCACTTCT TCTCCACCT TGACAAGTAT GTATCATTTCT AGACTGTGTC ATGAGTCTT CAGGACGTA AGAATACAA GACCTCTTTC
 1001 TGGAGGGGGG GTCACCAAGA CTTTCTCTGG CTGGCTGGG CCTTCCCTC AACCTTCTG ACATCTGCAG CCTCTTCAT TCTTGCCCTC ATTCTCTGGC
 ACCTCCCCC CAGTGTCTT GAAAGAGACC GACCGACCCG GGAAGGGAG TTGAAAGAC TGTAGACGTC GGAGAGAGTA AGAACGGAAG TAAGAGACCG
 1101 CCTGAACCGA GAGGTGATA TCAGATAGC TGACAGAAGA TGACCAGCA CACTGTCTG GTTGAACC AGAGGGACA ATAAAAACC CTGATTCTGG
 GGAATTGGCT CTCCCACTAT AGTCTATCG ACTGCTTCT ACTGCTCCGT GTGACAGGAC CAACTTTGG TCTCCCTGT TATTTTTGG GACTAAGACC
 1201 TCTCTACTCA CATAAAAAGA AGCTTGGA CATTAGTGG GAAGAGTTG CTACTAATA ACATACCTTG TAATTTCATC TTAATTAAAA TATACTTCTC
 AGAGATGAGT GTATTTTCT TCGAACACTT GTAATTAC CTTCTCTAAC GATGATTTAT TGTATGGAAC ATTAAGTAG AATTAAATTTT ATATGAAGAG
 1301 TATATTATAT ATTTTAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAATGC GGCCGCAAC TTATTCATT TAGGA
 ATATAATATA TAAATTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTGTACG CCGCGCTTC AATAAGTAA ATCCT

^insert ends

Fig. 9b

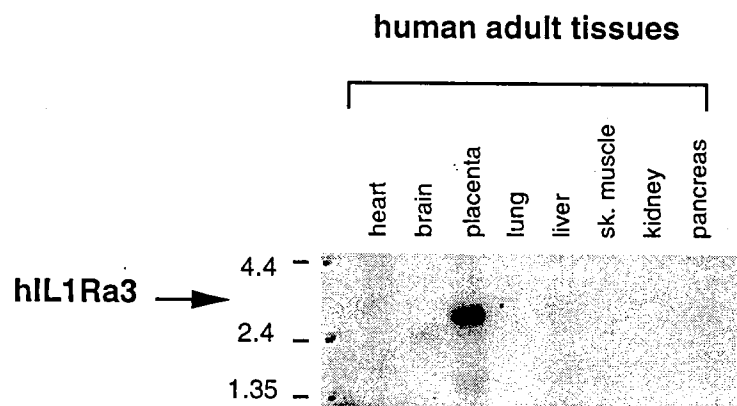
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 CCTCGGACGA AAGATGAATC CAGAGTTTAA AAGGTGGAA CAGAAACGGA TTTTAAAGGA CGACAATATA AGTTTATTC CAGATGTATG ACACCTCGAG

 101 ATGATGTTTC TGAGTGGGGC ACTATGCTTC CGAATGAAGG ATTGAGCCTT GAAGTACTG TATCTGCACA ATACCAAGCT GCTGGCTGGA GGACTGCACG
 TACTACCAAG ACTCACCCCG TGATACGAAG GCTTACTTCC TAAGTCGAA CTTCATGAC ATAGACGTGT TATTGTCGA CGACCGACT CCTGACGTGC
 1 M M V L S G A L C F R M K D S A L K V L Y L H N Q L L A G G L H A
 orf

 201 CAGAGAAGGT CATTAAGGT GAGAGATCA GTGTGTCCC AAATCGGGCA CTGATGCCA GTCTGTCCC TGTATCCTG GCGTTCAG GAGGAAGCCA
 GTCTCTTCCA GTAATTCCA CTCCTCTAGT CACAACAGGG TTTAGCCCGT GACCTACGT CAGACAGGGG ACAGTAGAC CCGCAAGTTC CTCCTTCGGT
 35 E K V I K G E E I S V V P N R A L D A S L S P V I L G V Q G G S Q

 301 GTGCTATCT TGTGGACAG AGAAAGGCC AATTCTGAAA CTGAGCCAG TGAACATCAT GGAGCTTAC CTCGGGGCCA AG
 CACGATAGA ACACCTGTG TCTTCCCG TTAAGACTTT GAACTCGTC ACTGTAGTA CCTCGAGATG GAGCCCGGT TC
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A



B

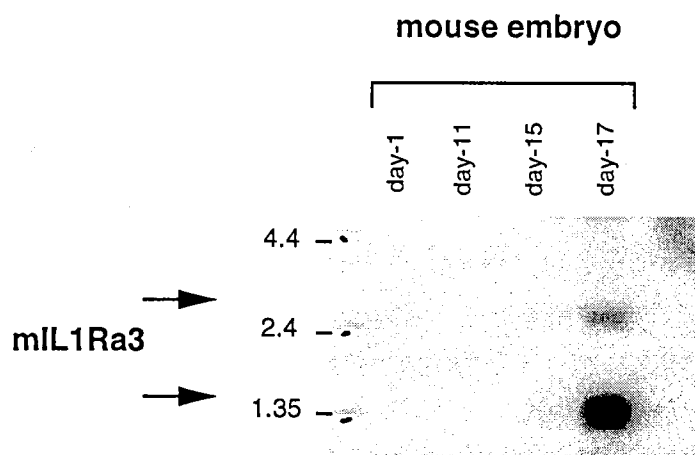


Fig. 11

hIL1Ra	1	MEICRGLRS	ITLLFLFHSETIC	R	P	S	G	R	K	S	S	K	M	Q	A	I	W	D	V	N	Q	K	T	F	Y	L																									
hIL1Rabeta	1	MRGTPGDADGGG	R	A	V	Y	Q	S	M	C	K	P	I	T	G	T	I	N	D	L	N	Q	Q	V	W	T	L																							
hIL1Ra1	1	C	R	G	P	K	V	K	N	L	N	P	K	K	F	S	I	H	D	Q	D	H	K	V	L	V	L																						
hIL1Ra2	1	MRGTPGDADGGG																						
hIL1Ra3	1																						
mIL1Ra3	1																					
hIL1Ra	51	R	N	N	Q	L	V	A	G	Y	L	Q	G	P	..	N	V	N	L	E	E	K	I	D	V	V	P	I	E	P	H	A	L	F	L	G	I	H	G	G	K	M	C	L	S			
hIL1Rabeta	38	Q	G	Q	N	L	V	A	V	P	R	S	D	S	V	T	P	V	T	V	A	V	I	T	C	K	Y	P	E	A	L	E	Q	G	R	G	D	P	I	Y	L	G	I	Q	N	P	E	M	C	L	Y
hIL1Ra1	27	D	S	G	N	L	I	A	V	P	D	K	N	..	Y	I	R	P	E	I	F	F	A	L	A	S	S	L	S	S	A	S	A	E	K	G	S	P	I	L	L	G	V	S	K	G	E	F	C	L	Y
hIL1Ra2	13		
hIL1Ra3	22	H	N	N	Q	L	L	A	G	G	L	H	A	G	..	K	V	I	K	G	E	E	I	S	V	V	P	N	R	W	L	D	A	S	L	S	P	V	I	L	G	V	Q	G	G	S	Q	C	L	S	
mIL1Ra3	22	H	N	N	Q	L	L	A	G	G	L	H	A	E	..	K	V	I	K	G	E	E	I	S	V	V	P	N	R	A	L	D	A	S	L	S	P	V	I	L	G	V	Q	G	G	S	Q	C	L	S	
hIL1Ra	94	C	V	K	S	G	..	D	E	T	R	L	Q	L	E	A	V	N	I	T	D	L	S	E	N	R	K	..	Q	D	K	R	F	A	F	I	R	S	D	S	G	P	T	T	S	F	E	S	A	A	
hIL1Rabeta	88	C	E	K	V	G	..	E	Q	P	T	L	Q	L	K	E	Q	K	I	M	D	L	Y	G	Q	P	E	..	P	V	K	P	F	L	F	Y	R	A	K	T	G	R	T	S	T	L	E	S	V	A	
hIL1Ra1	76	C	D	K	D	K	G	Q	S	H	P	S	L	Q	L	K	K	E	K	L	M	K	L	A	A	Q	K	E	S	A	R	R	P	F	I	F	Y	R	A	Q	V	G	S	W	N	M	L	E	S	A	
hIL1Ra2	53	C	E	K	V	G	..	E	Q	P	T	L	Q	L	K	E	Q	K	I	M	D	L	Y	G	Q	P	E	..	P	V	K	P	F	L	F	Y	R	A	K	T	G	R	T	S	T	L	E	S	V	A	
hIL1Ra3	70	C	G	V	G	..	Q	E	P	T	L	T	L	E	P	V	N	I	M	E	L	Y	L	G	A	K	..	E	S	K	S	F	T	F	Y	R	R	D	M	G	L	T	S	S	F	E	S	A			
mIL1Ra3	70	C	G	T	E	..	K	G	P	I	L	K	L	E	P	V	N	I	M	E	L	Y	L	G	A	K	..	E	S	K	S	F	T	F	Y	R	R	D	M	G	L	T	S	S	F	E	S	A			
hIL1Ra	141	C	P	G	W	F	L	C	T	A	M	E	A	D	Q	P	V	S	L	T	N	M	P	D	E	G	..	V	M	V	T	K	F	Y	F	Q	E	D	E	
hIL1Rabeta	135	F	P	D	W	F	I	A	S	S	K	R	D	Q	P	I	I	L	T	S	E	L	G	K	S	Y	N	..	T	A	F	E	L	N	I	N	D	
hIL1Ra1	126	H	P	G	W	F	I	C	T	S	C	N	C	N	E	P	V	G	V	T	D	K	F	E	N	R	K	H	I	E	F	S	F	Q	P	V	C	K	A	E	M	S	P	S	E	V	S	D			
hIL1Ra2	100	F	P	D	W	F	I	A	S	S	K	R	D	Q	P	I	I	L	T	S	E	L	G	K	S	Y	N	..	T	A	F	E	L	N	I	N	D		
hIL1Ra3	116	Y	P	G	W	F	L	C	T	V	P	E	A	D	Q	P	V	R	L	T	Q	L	P	E	N	G	G	W	N	A	P	I	T	D	F	Y	F	Q	Q	C	D		
mIL1Ra3	116	Y	P	G	W	F	L	C	T	S	P	E	A	D	Q	P	V	R	L	T	Q	I	P	E	D	P	A	W	D	A	P	I	T	D	F	Y	F	Q	Q	C	D		

Fig. 12

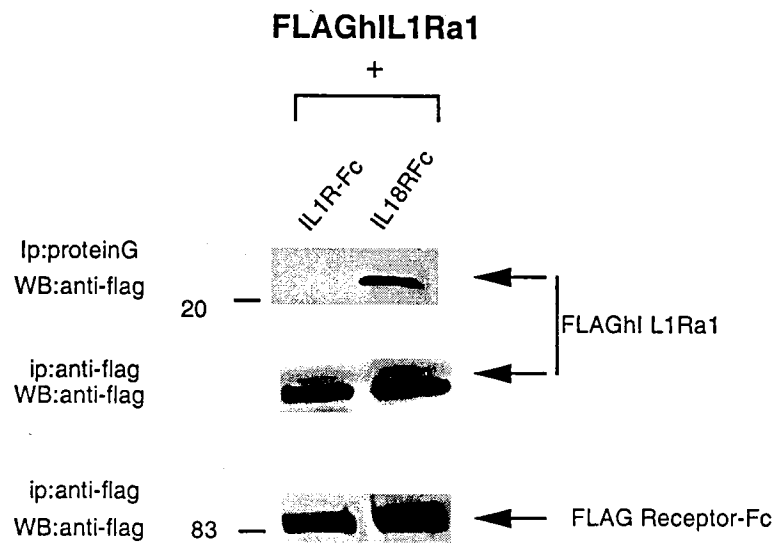


Fig.13

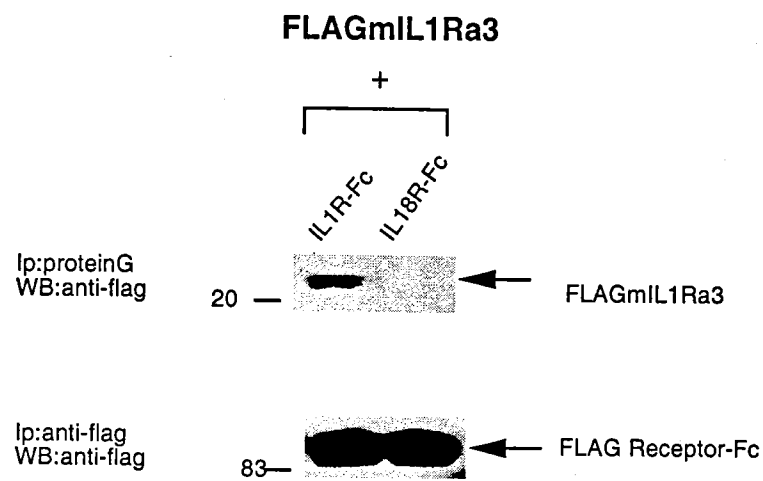


Fig 14